



SEQUENCE LISTING

10> Kimble, Judith E
Blelloch, Robert H

<120> Agent and Method for Modulating Cell Migration

5 <130> 960296.95386

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	Asn Cys Pro Tyr Glu Trp Val Pro Gly Asp Trp Gln Thr Cys Ser Lys	
	1795 1800 1805	
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	Ser Cys Gly Glu Gly Val Gln Thr Arg Glu Val Arg Cys Arg Arg Lys	
	1810 1815 1820	
	att aat ttt aac tca acc att cca att ata ttt atg ctc gaa gat gaa	5520
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	1825 1830 1835 1840	
	cca gct gta cca aaa gag aaa tgt gaa ctt ttc cca aaa cca aat gaa	5568
	Pro Ala Val Pro Lys Glu Lys Cys Glu Leu Phe Pro Lys Pro Asn Glu	
	1845 1850 1855	
35	tct caa acg tgc gaa ctt aac cca tgc gat tcg gaa ttc aaa tgg agt	5616
	Ser Gln Thr Cys Glu Leu Asn Pro Cys Asp Ser Glu Phe Lys Trp Ser	
	1860 1865 1870	
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	Phe Gly Pro Trp Gly Glu Cys Ser Lys Asn Cys Gly Gln Gly Ile Arg	
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	Arg Arg Arg Val Lys Cys Val Ala Asn Asp Gly Arg Arg Val Glu Arg	
	1890 1895 1900	

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	Arg Asn Cys Leu Pro Ser Thr Cys Gln Glu Leu Lys Ser Gln Asn Val	
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	aag gct aaa gat gga aat tac act att ctt ctt gac gga ttc act att	5856
	Lys Ala Lys Asp Gly Asn Tyr Thr Ile Leu Leu Asp Gly Phe Thr Ile	
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10	gaa att tat tgt cat cga atg aat tca acc att cct aaa gct tat ttg	5904
	Glu Ile Tyr Cys His Arg Met Asn Ser Thr Ile Pro Lys Ala Tyr Leu	
	1955 1960 1965	
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	Ile Tyr Pro His Thr Cys Pro Phe Asn Gly Asp Arg Asn Asp Ser Cys	
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	His Cys Ser Glu Asp Gly Asp Ala Ser Ala Gly Leu Thr Arg Phe Asn	
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	Lys Val Arg Ile Asp Leu Leu Asn Arg Lys Phe His Leu Ala Asp Tyr	
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	Thr Phe Ala Lys Arg Glu Tyr Gly Val His Val Pro Tyr Gly Thr Ala	
	2035 2040 2045	
	ggt gat tgc tac agt atg aaa gat tgt cca cag gga ata ttc tca att	6192
	Gly Asp Cys Tyr Ser Met Lys Asp Cys Pro Gln Gly Ile Phe Ser Ile	
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	gat tta aaa tct gct ggt ctg aaa tta gtt gac gat ctg aat tgg gag	6240
	Asp Leu Lys Ser Ala Gly Leu Lys Leu Val Asp Asp Leu Asn Trp Glu	
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	gat caa ggt cat cga aca tcc tct cga atc gat cgt ttt tat aac aat	6288
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	Ala Lys Val Ile Gly His Cys Gly Gly Phe Cys Gly Lys Cys Ser Pro	
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	Glu Arg Tyr Lys Gly Leu Ile Phe Glu Val Asn Thr Lys Leu Leu Asn	
	2115 2120 2125	

cat gtg aaa aat ggt gga cac att gat gat gaa ttg gat gat gat ggt 6432
His Val Lys Asn Gly Gly His Ile Asp Asp Glu Leu Asp Asp Asp Gly
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Ser Gly Thr Ile Ser Glu Phe Ser Ser Asp Val Leu Phe Ser Arg Ala
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Lys Tyr Ser Gly Val Pro Val His His Ser Arg Trp Arg Gln Asp Ala
50 55 60
Gly Ile His Val Ile Asp Ser His His Ile Val Arg Arg Asp Ser Tyr
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25 Gly Arg Arg Gly Lys Arg Asp Val Thr Ser Thr Asp Arg Arg Arg Arg
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Leu Gln Gly Val Ala Arg Asp Cys Gly His Ala Cys His Leu Arg Leu
100 105 110
Arg Ser Asp Asp Ala Val Tyr Ile Val His Leu His Arg Trp Asn Gln
30 115 120 125
Ile Pro Asp Ser His Asn Lys Ser Val Pro His Phe Ser Asn Ser Asn
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Phe Ala Pro Met Val Leu Tyr Leu Asp Ser Glu Glu Glu Val Arg Gly
145 150 155 160

35 Gly Met Ser Arg Thr Asp Pro Asp Cys Ile Tyr Arg Ala His Val Lys
165 170 175
Gly Val His Gln His Ser Ile Val Asn Leu Cys Asp Ser Glu Asp Gly
180 185 190

Leu Tyr Gly Met Leu Ala Leu Pro Ser Gly Ile His Thr Val Glu Pro
 195 200 205
 Ile Ile Ser Gly Asn Gly Thr Glu His Asp Gly Ala Ser Arg His Arg
 210 215 220
 5 Gln His Leu Val Arg Lys Phe Asp Pro Met His Phe Lys Ser Phe Asp
 225 230 235 240
 His Leu Asn Ser Thr Ser Val Asn Glu Thr Glu Thr Thr Val Ala Thr
 245 250 255
 10 Trp Gln Asp Gln Trp Glu Asp Val Ile Glu Arg Lys Ala Arg Ser Arg
 260 265 270
 Arg Ala Ala Asn Ser Trp Asp His Tyr Val Glu Val Leu Val Val Ala
 275 280 285
 Asp Thr Lys Met Tyr Glu Tyr His Gly Arg Ser Leu Glu Asp Tyr Val
 290 295 300
 15 Leu Thr Leu Phe Ser Thr Val Ala Ser Ile Tyr Arg His Gln Ser Leu
 305 310 315 320
 Arg Ala Ser Ile Asn Val Val Val Val Lys Leu Ile Val Leu Lys Thr
 325 330 335
 20 Glu Asn Ala Gly Pro Arg Ile Thr Gln Asn Ala Gln Gln Thr Leu Gln
 340 345 350
 Asp Phe Cys Arg Trp Gln Gln Tyr Tyr Asn Asp Pro Asp Asp Ser Ser
 355 360 365
 Val Gln His His Asp Val Ala Ile Leu Leu Thr Arg Lys Asp Ile Cys
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 25 Arg Ser Gln Gly Lys Cys Asp Thr Leu Gly Leu Ala Glu Leu Gly Thr
 385 390 395 400
 Met Cys Asp Met Gln Lys Ser Cys Ala Ile Ile Glu Asp Asn Gly Leu
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 30 Ser Ala Ala Phe Thr Ile Ala His Glu Leu Gly His Val Phe Ser Ile
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 Pro His Asp Asp Glu Arg Lys Cys Ser Thr Tyr Met Pro Val Asn Lys
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 Asn Asn Phe His Ile Met Ala Pro Thr Leu Glu Tyr Asn Thr His Pro
 450 455 460
 35 Trp Ser Trp Ser Pro Cys Ser Ala Gly Met Leu Glu Arg Phe Leu Glu
 465 470 475 480
 Asn Asn Arg Gly Gln Thr Gln Cys Leu Phe Asp Gln Pro Val Glu Arg
 485 490 495

	Arg	Tyr	Tyr	Glu	Asp	Val	Phe	Val	Arg	Asp	Glu	Pro	Gly	Lys	Lys	Tyr	500	505	510
	Asp	Ala	His	Gln	Gln	Cys	Lys	Phe	Val	Phe	Gly	Pro	Ala	Ser	Glu	Leu	515	520	525
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	Val	Arg	Leu	Ala	Pro	Glu	Ser	Leu	Thr	Lys	Ile	Asp	Gly	Gln	Trp	Gly	580	585	590
	Asp	Trp	Arg	Ser	Trp	Gly	Glu	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	595	600	605
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	Lys	Tyr	Cys	Val	Gly	Gln	Arg	Glu	Arg	Tyr	Arg	Ser	Cys	Asn	Thr	Gln	625	630	635 640
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	Thr	Leu	Arg	Arg	Asp	Lys	Cys	Gly	Val	Cys	Gly	Gly	Asp	Asp	Ser	Ser	740	745	750
	Cys	Lys	Val	Val	Lys	Gly	Thr	Phe	Asn	Glu	Gln	Gly	Thr	Phe	Gly	Tyr	755	760	765
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	Gln	Lys	Gly	Tyr	Asn	Asn	Met	Lys	Glu	Asp	Asp	Asn	Tyr	Leu	Ser	Leu	785	790	795 800

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